Classification of Life

NGSS Performance Expectations	MS-LS4-2 Apply scientific ideas to construct an explanation for the anatomical similarities and differences among modern organisms and between modern and fossil organisms to infer evolutionary relationships. HS-LS1-2 Develop and use a model to illustrate the hierarchical organization of interacting systems that provide specific functions within multicellular organisms.

The content and activities in this topic will work towards building an understanding of how scientists organize and classify living organisms.

Humans constantly try to organize information about the world around them in meaningful ways. One way that we try to accomplish this is by classifying things into different groups based on how things are alike and different. Think about some of the things classified around your home or school and the methods used to classify non-living things.

One branch of biology, called taxonomy, focuses on the classification of living things. **Taxonomy** is the study of relationships between living things and the formal classification of organisms into groups based upon those hypothesized relationships. Organisms are classified based upon their similarities and differences.

Think about your own biological relatives. Your biological relatives include those that you are related to by birth, for example parents, brothers, sisters, cousins, aunts, uncles, and grandparents. When two organisms are related, it means that they share a common ancestor. The more recent the ancestor, the more closely related the organisms are. Your closest relatives would be siblings (brothers and sisters) because you share the closest common ancestor—a parent. Your cousins are not as closely related to you because your common ancestor is farther away—a grandparent (your parent's parent).

Taxonomy takes into account the functional similarity as well as genetic similarity of individuals. Human beings are mammals and are more closely related to primates, such as apes, than to other mammals such as dogs. Humans and apes share functional similarity in hands and facial features when compared to a dog's face and paws. This fact supports the idea that humans share a closer common ancestor to apes than dogs.

Although scientists have described nearly 2 million species on Earth, this number is estimated to only be a small proportion of the actual number of species alive today. There is an extensive fossil record of plants and animals that lived in the past and that may be distant relatives of living species. The relationships between all of these different extant and extinct organisms on our planet are amazingly intricate and complex. Scientists are interested in classifying the many species currently living on Earth, as well as those that are no longer living. They are also interested in studying the evolutionary mechanisms that generate and maintain new species. Some species may look very similar to each other, so it is important for scientists to establish specific criteria for what distinguishes one species from another.

Classification

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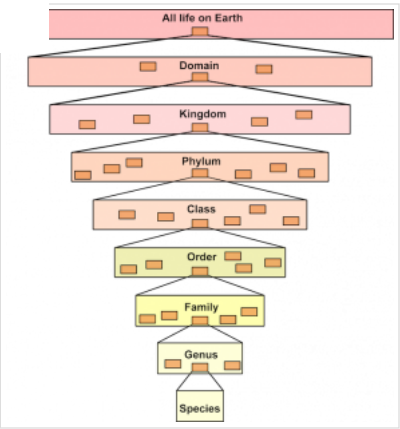

Fig. 1.9. This diagram illustrates the nested hierarchy used in modern biological classification.

Image adapted from Dosto, Wikimedia Commons

In 1753, a Swedish biologist named Carl Linnaeus (also known as Carl von Linné) proposed a universal system for classifying and naming animals and plants. Scientists still use this Linnean system to classify living things. A hierarchical system, it works like a series of nesting boxes (Fig. 1.9). The largest box is the domain, and all the other levels of classification fit within the domains.

There are three domains that include all the living things on Earth. The domains are Bacteria, Archaea, and Eukarya. Bacteria and Archaea are all single-celled microorganisms that do not have DNA contained within a nucleus. Most of the Archaea live in extreme environments. The Bacteria and Archaea were once grouped together as a single kingdom (called Monera), but scientists later discovered that the Archaea were distinctly different. Archaea are more similar to Eukarya than to Bacteria.

Fig. 1.10. Hawaiian goose or *nēnē* (*Branta sandvicensis*), Kīlauea Point, Kaua'i, Hawai'i.

Image courtesy of Jörg Hempel, Wikimedia Commons

The domain Eukarya includes all organisms that have DNA contained within a nucleus. Within the domain Eukarya, there are four kingdoms: Protista, Fungi, Plantae, and Animalia. Organisms with similar characteristics are grouped within these broad kingdoms.

Organisms are usually grouped together based on their unique characteristics. The classification of an organism often provides useful information about its evolutionary history and which other organisms are related to it. For example, the Hawaiian goose or *nēnē* (*Branta sandvicensis*; Fig. 1.10) is classified as shown in Table 1.9.

Table 1.9. Classification of the Hawaiian goose or *nēnē* bird (*Branta sandvicensis*). Table includes the meaning and the key characteristics of the taxon.

Taxon	Classification	Meaning	Key characteristics
Domain	Eukarya	true nucleus	DNA is contained within a nucleus.
Kingdom	Animalia	animal	Must eat other things.
Phylum	Chordata	has a notochord	Notochord supporting dorsal nerve cord, gill slits
Class	Aves	bird	Has feathers and hollow bones.
Order	Anseriformes	waterfowl	Webbed front toes
Family	Anatidae	swans, ducks & geese	Broad bill, keeled sternum, feathered oil gland
Genus	*Branta*	Brent or black geese	Bold plumage, black bill and legs
Species	*sandvicensis*	from the Sandwich Islands	The Sandwich Islands is an old name for Hawai'i. This is the Hawaiian goose or *nēnē*.

At each level of hierarchy listed in Table 1.9, more information about the *nēnē* is revealed. If the classification of the nēnē is imagined as a series of nested boxes (Fig. 1.9), the first box is the domain Eukarya box. All organisms in Eukarya (often referred to as eukaryotes) have DNA contained in a nucleus rather than in the cytoplasm like the domains Prokarya and Archaea.

Next is the kingdom Animalia box. Everything in this box must consume other organisms to survive. Other kingdoms within Eukarya, like the kingdom Plantae, have organisms that can make their own food.

Within the kingdom Animalia box, there are several other boxes, each labeled as a different phylum. One is the phylum Chordata box. This box contains everything that has a notochord, gill slits, and a dorsal nerve cord.

The phylum Chordata box contains many classes, one of which is the class Aves. Aves are the birds, with feathers and hollow bones.

The class Aves box includes the box labeled order Anseriformes, the waterfowl that are grouped together due to their webbed front toes.

The order Anseriformes box contains two family boxes. One of these is the family Anatidae—the swans, ducks, and geese that have a broad bill, a keeled sternum, and other unique features.

The family Anatida box contains the genus *Branta*. Geese in the genus Branta are noted for bold plumage and legs and bills that are black in color.

The genus box *Branta* holds the species *sandvicensis*. By examining each level of classification, it becomes clear that *Branta sandvicensis* is a Hawaiian goose with a black broad bill, legs, webbed toes, feathers, hollow bones, and a notochord. It must also eat other things. Note that several other species found in Hawai'i are given the species name *sandvicensis* because Sandwich Islands is an older European name for the Hawaiian Islands. However, no other organism on earth is given the genus *Branta* and the species *sandvicensis*. *Branta sandvicensis* is reserved only for the *nēnē*.

The classification system tells something about the evolutionary relationships among species. Moving down through each level of classification, the number of species in the group decreases (Table 1.10). Two species within the same genus likely share a recent common ancestor in their evolutionary history. These two species would be more closely related to each other than two species classified into different families.

Table 1.10. The number species decreases in each group moving down the levels of classification.

Kingdom Animalia: Over 1.6 million species
Phylum Chordata (chordates): Approximately 51,500 species
Class Sarcopterygii (includes lobe-finned fishes): Approximately 32,000 species including 2 coelacanths, 6 lungfishes, and all four-limbed vertebrates
Order Coelacanthiformes (coelacanths): 2 species
Family Latimeriidae: 2 species
Genus *Latimeria*: 2 species
Species *chalumnae* and *menadoensis*

The levels of classification might also provide information on the evolutionary history of a species or other taxonomic group. Such is the case with the coelocanths *Latimera* spp.) whose classification is detailed in Table 1.10. West Indian ocean coelacanth (*Latimeria chalumnae*; Fig. 1.10.1) and its sister species the Indonesia coelacanth (*Latimera menadoensis*) are the only living members of their genus (*Latimera*). They are also the only living members of their family (Latimeriidae) and of their order (Coelacanthiformes). All other species belonging to these levels of classification are now extinct.

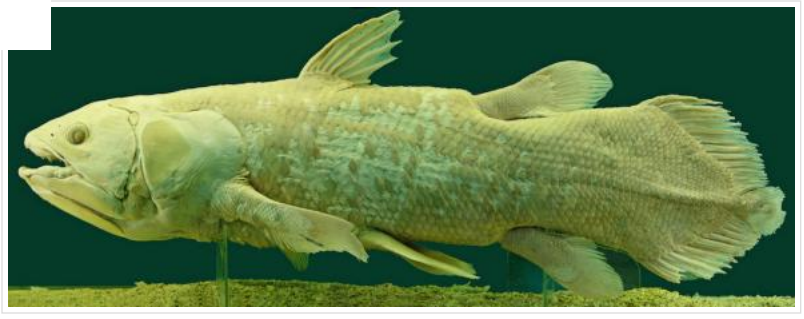

Fig. 1.10.1. Preserved specimen of West Indian ocean coelacanth (*Latimera chalumnae*), Vienna Natural History Museum, Austria

Image courtesy of Alberto Fernandez Fernandez, Wikimedia Commons

Coelacanths are also some of the very few surviving fish species within the class Sarcopterygii, a group known as the lobe-finned fishes. All four-limbed vertebrate animals—amphibians, reptiles, birds, and mammals—also belong to class Sarcopterygii. The coelacanths, and the six species of lung fish, are more closely related to each other and to the four-limed vertebrates than to other fishes. For this reason, the

coelacanth offers a rare glimpse into the evolutionary history of vertebrate animals and their limb-development.

Classification systems are used in many ways. Compare the classifications shown in Fig. 1.11 and Fig. 1.12. Most people know something about water vehicles, so it is not necessary to say that a speedboat has a motor. In the same way, there is general knowledge that a tuna is classified as a fish. So, a tuna can be described without needing to say that it is a fish because. Thus, if we make the statement that a skipjack tuna is caught while fishing in a speedboat, many details can be left out of the description because there is general, underlying knowledge of the classification of boats and tuna.

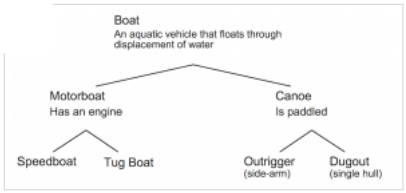

Fig. 1.11. Example classification scheme for small boats

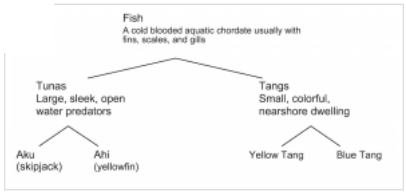

Fig. 1.12. Example classification scheme for fish

Scientific Nomenclature

The scientific name of the Hawaiian goose or *nēnē*—its genus and species name—are written in italics. This use of italics is part of the rules that the scientific community has developed for the naming of organisms. There are three main codes that govern the naming of organisms.

- The International Code of Zoological Nomenclature governs the naming of animals.
- The International Code of Botanical Nomenclature governs the naming of plants and fungi.
- The International Code of the Nomenclature of Bacteria governs the naming of bacteria.

The following are some basic nomenclatural rules that apply to all three codes:

1. In general, organisms are identified by their binomial name, consisting of the genus and species names.
2. The genus name is always capitalized, whereas the species name is not. Both names are always *italicized* or underlined.
3. Genus names can be abbreviated by their first letter, but species names cannot. For example, after initially referring to the leafy sea dragon, *Phyllopteryx eques*, it could subsequently be written *P. eques*.
4. Unknown species are referred to with the abbreviation sp. For example, a seahorse of an unknown species in the genus *Hippocampus* would be written *Hippocampus* sp. Note that sp. is not italicized.
5. Some genera have more than one species in them. To refer to multiple species within the same genus, the genus name is followed with the abbreviation spp. A group of seahorses all in the genus *Hippocampus* could be written *Hippocampus* spp. Note that spp. is not italicized.

Scientific names are useful outside of science. Common names vary from place to place, and the scientific nomenclature system helps eliminate confusion. For example, the fish called *mahi-mahi* in Hawai'i has at least three common names; it is called *dolphinfish* in Florida, but it is called *dorado* in the Caribbean and Central America. This example also brings up another problem with common names. Notice that one of the common names for this fish uses the word dolphin, which is also the common name of a marine mammal. Imagine the confusion that this could cause if someone from Hawai'i were to visit a Florida restaurant and see dolphin on the menu—they might think that the restaurant serves the mammal dolphin, rather than the dolphinfish.

Scientific names are also valuable in navigating the classification system. The classification system provides great deal of information about the characteristics of organisms. Using scientific names can therefore act as a shorthand method for describing a plant or animal.

For example, following a whale stranding along the Maui coastline, an observer might record this information:

Date: February 2, 2016

Location: Lahaina, Maui

Observer: Sarah Anole

Time: 10:00 AM

Weather: Partly cloud, with good visability

Behavior Observation: large multicellular organism washed up on shore, and appears to have stranded itself

Organism Identification: The organism appears to be heterotrophic. The large body—over 7 meters long—is streamlined with a shortened neck. The front limbs are paddle shaped and are almost a third of the body length. They are largely white and have knobs on the leading edge. The tail is flattened and has scalloped horizontal flukes. There is a small hump shaped dorsal fin. Rather than teeth, there is in the mouth a set of short and broad black plates with black bristles hanging from the upper jaw. There are deep grooves in the skin, running down the throat and chest. They eyes are very small. There is a pair of external nostrils (a double blowhole) at the top of the head.

This is all information needed to identify the organism and avoid mixing it up with other similar organisms. Of course, when reporting the mammal stranding to her supervisor, the observer will report stranding of a *Megaptera novaeangliae*, which is the species name that describes the humpback whale. There is only one species in Hawai'i that meets all of the qualities described above. The scientific name *Megaptera novaeangliae* encompasses all of the described features.

Most binomial names are Latin terms. However, some binomial names are Greek, and some are derived from the names of their discoverers or other scientists. When Carl Linneaus developed his classification system, almost all educated people were trained in Latin and Greek. No matter what country they came from, people could communicate with one another using these languages. Because Latin and Greek were the common languages of scientists, Latin and Greek were used to develop a universal classification system. Even today, the English language has many words that were originally Latin or Greek in origin.

Latin and Greek terminology is also useful because it tends to be very descriptive of the species in question (Table 1.11). For example, consider the great white shark. This animal is referred to as a "white pointer" in Australia and a "grey pointer" in South Africa. However, the great white shark is universally known by its scientific name of *Carcharodon carcarias* around the world. The root word –*odon* sounds like the familiar type of dentist—the orthodontist. In fact, *odon* is a root word that means tooth. *Carcharo-* means jagged. When put together, the word *Carcharodon* means jagged-toothed shark. The person who named this shark incorporated this observational fact within the name.

Table 1.11. A partial listing of Greek and Latin terms (roots, prefixes, and suffixes)

a- without (G)	*endo*, *ento-* within (G)	*mis-* less, wrong (L)	*tera* monster (G)
ab- away (L)	*eu-* good, true (G)	*mono-* one (G)	*trans-* over, across (L)
acanth spine or thorn (L)	*extra-* beyond (L)	*-morph* shape or form (G)	*tri* three (L)
*acro-*top or end (G)	*fer-* to carry (L)	*mov* to move (L)	*tricho* hair (G)
acu needle (L)	*flavi* yellow (L)	*mycto* nose (G)	*un-* not (L)
ala wing (L)	*-form* shape (L)	*myo* muscle (G)	*uni* one (L)
alb white (L)	*fort* strong (L)	*nect* swimming (G)	*vac* empty (L)
alt high (L)	*galax* milky (G)	*nema* thread (G)	*vest* to adorn (L)
ambi around, both (L)	*gaster* stomach (G)	*neo* new (G)	*voc* voice (L)
amphi both, around (G)	*geo* earth (G)	*omni* all (L)	*xena* strange (G)
anguilla eel (L)	*giga* giant (G)	*onco* hook (G)	*xiph* sword (G)
anthrop man (G)	*gladius* sword (L)	*op-* against, toward (L)	
apo- away from, off (G)	*gnath* jaw (G)	*opt-*eye (L)	
aqua water (L)	*grav-*heavy (L)	*orecto* stretched (G)	
arch, archi chief, to rule (G)	*gymn* naked (G)	*osmer* odor (G)	

archa old, ancient (G)	*halo* salt (G)	*osteo* bone (G)	
argent silver (L)	*hemi-* half (G)	*oxy* sharp (G)	
arthro a joint (G)	*hetero* various, different (G)	*paleo* ancient (G)	
aspis shield (G)	*holo-* whole (G)	*pan* all, every (G)	
aster star (G)	*homo-* same (G)	*para-* beside, beyond (L)	
auric gold (L)	*hydro* water (G)	*ped* foot (L)	
auto self (G)	*hyo* pig, hog (G)	*pegas* strong (G)	
barb beard (L)	*hyper-* above, beyond (G)	*penta* five (G)	
bathy deep (G)	*hypo-* under, less than (G)	*peri-* around, about (G)	
ben, *bon* good (L)	*ict* fish (G)	*petro* rock (G)	
bi two (L)	*in*, *ir*, *im*, *il* - not, without (L)	*phil* love (L)	
brachi arm (G)	*inter-* between (L)	*photo-* light (G)	
branch gill (G)	*intro-* within (L)	*phyllo* leaf (G)	
callo beautiful (L)	*iso-* equal (G)	*pimelod* fat, soft (G)	
capit head (L)	*juven* young (L)	*pinna* wing, feather (L)	
carchar jagged (G)	*lati* side (L)	*platy* flat (G)	
cell to project (L)	*lev* to raise (L)	*plect* twisted (G)	
cerat horn (G)	*liber* free (L)	*plur-* more (L)	
circ, *circum-* around (L)	*lingu* tongue (L)	*poly-* many (G)	
clad branch (G)	*lith* stone (G)	*pre-* before (L)	
co, *con*, *com-* together (L)	*loph* crest (G)	*prim* first (L)	
coelo hollow (G)	*lucio* light (L)	*pseudo* false, fake (G)	
contra against (L)	*macro-* long, large (G)	*pyr* fire (L)	
cor, *cour* heart (L)	*magn*, *mag*, *meg*, *maj-* great (L)	*quad* four (L)	
corp body (L)	*mal* - bad (L)	*retro-* backward, behind (L)	
cteno comb (G)	*man* hand (L)	*rhyncho* beak (G)	
dasy hairy (G)	*medi* middle (L)	*scope* to see (L)	
deca ten (G)	*mega-* great (G)	*semi-* half (L)	
dent tooth (L)	*melano* black (G)	*sol* alone (L)	
derm skin (G)	*micro-* small (G)	*somn* sleep (L)	
di two (G)	*mill-* thousand (L)	*sten* narrow (G)	
dys difficult, bad (G)	*mimo* to imitate (G)	*stephano* crown (G)	
echino prickly (G)	*mira* strange (L)	*sub* - under, below (L)	
ecto- outside of (G)		*super*, *supra-* above (L)	
		syn, *sym-* together (G)	
		tac silent (L)	
		taenio ribbon (G)	
		tele far off (G)	

ACTIVITY

What's in a Name?

Create names for 15 species of sharks and compare them with the actual scientific and common names.

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Identification Keys

Although more than two million different species have been identified by scientists, millions more are likely still undiscovered. A **dichotomous key** is a tool used by scientists to help them identify organisms that are already classified and described. The key presents a series of choices that leads the user to the identification of the organism. The series of choices is similar to a series of contrasting hypotheses that are tested by examining the organism to disprove one hypothesis and support the other.

A detailed description exists for every organism with a scientific name. The final step in any identification should be to compare the specimen to a species description. It is important to make this comparison because it is possible to misinterpret the information presented, and it is also possible that the specimen was not in the key or that the specimen is even a new, undescribed species.

A **diagnosis** is the comparison of the organisms' description with the specimen. If the diagnosis does not contradict what is known about the specimen, the identification is supported. For example, if the specimen was caught in water one meter deep, but the diagnosis says that the organism only lives at depths of 150 meters or more, there may be an error in the identification. If this happens, test other hypotheses by working back through the key and trying to determine where a wrong decision was made.

Like following directions to a rural house in the country, a dichotomous key will almost always lead to a species name (just as a road usually leads to a house). But what if a wrong choice was made because a certain feature was missed, or what if the specimen is of a different (or new) species that shares many features with the one in the key? The best way to ensure that the organism is correctly identified is to confirm that it matches in every way with the species description.

Most keys are regional, based on the animals of the place where the key was developed. It is important not to use a key for the fishes of Illinois when trying to identify a fish caught in Hawai'i. Most keys also have a section that only identifies the families in the region. This is a good place to start because families are often easier to separate and identify than individual species. It is also important to compare the final identification to a guidebook or other source in case the key did not contain the specimen in question.

ACTIVITY

Identifying Butterflyfish Using Dichotomous Keys

Use a dichotomous key to identify butterflyfish species

Classification Changes

The goal of biological classification is to group organisms together in terms of their relatedness to one another. There is a long-running debate within the scientific community about whether the Linnean system should be revised to better show relatedness. There are several arguments for revision:

- The Linnean system tends to use only superficial characteristics.
- The Linnean system groups things together too frequently.
- Use of a standardized system (domain, kingdom, phylum, etc.) does not accurately reflect relationships between organisms and can thus lead to implied relationships that do not exist.
- Classification should be based on DNA or genetic information.

Phylogenetic Trees

The phylogenetic method of classification uses shared, unique characters—heritable features that vary between individuals. In contrast, the Linnean system is focused on ranking organisms in groups. Linnean groups share similar traits, but the groups often do not reflect evolution or levels of diversity. Phylogenetics, on the other hand, is focused on showing the evolutionary relationships between organisms.

A **phylogenetic tree** is a branching diagram used to show the evolutionary relatedness of organisms based on similarities and differences in their characteristics (Fig. 1.16 and Fig. 1.17). The length of the branches on a phylogenetic tree represents changes in characteristics over evolutionary time.

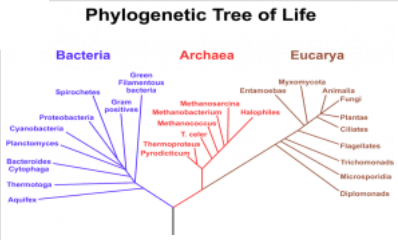

Fig. 1.16. This phylogenetic tree of life shows the three domains, which make up all of life on Earth. The length of the branches on phylogenetic trees represents evolutionary time.

Image courtesy of National Aeronautics and Space Administration (NASA) and Eric Gaba, Wikimedia Commons

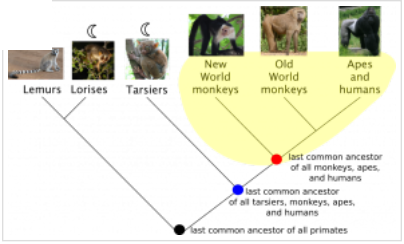
Lemurs
Lorises
Tarsiers
New World monkeys
Old World monkeys
Apes and humans
last common ancestor of all monkeys, apes, and humans
last common ancestor of all tarsiers, monkeys, apes, and humans
last common ancestor of all primates

Fig. 1.17. Phylogenetic trees show evolutionary relationships between species or other groups of organisms. A sample monophyletic group of monkeys, apes, humans, and their last common ancestor (red dot) is highlighted in yellow. A second potential monophyletic group could include those in yellow as well as the tarsiers and the last common ancestor of this larger group (blue dot).

Image by David Lin, courtesy of Lexicon, Alex Dunkel, Kalyan Varma, Steven G. Johnson, Muhammad Mahdi Karim, Brocken Inaglory, and Peter Coxhead from Wikimedia Commons, and motoz from Flickr

The term **synapomorphy** is used to describe shared, unique characteristics. Synapomorphies are present in organisms that are related through an ancestor who genetically passed the trait on to its descendants. Organisms outside the group do not have the synapomorphy. Phylogenetic trees show groups using synapomorphies.

A **monophyletic** group contains all of the descendants of a single common ancestor—an ancestor shared by two or more descendent lineages. In many cases, the common ancestor is unknown. For example, all members in the primate infraorder Simiiformes (shown in yellow in Fig. 1.17) share a single common ancestor (marked with a red dot). That means the relationship of all of the primates in this group is supported by synapomorphies. The more synapomorphies two species have in common, the more closely related they are hypothesized to be.

Sometimes scientists misinterpret groups as being monophyletic when they are not. A character that appears unique might evolve more than once in different groups, or it may be lost or reversed within a group. **Homoplasies** are similar characteristics, like the wings of birds and bats, that do not reflect relatedness. Bird wings and bat wings are not related because they evolved from different genetic origins, even if both types of wings serve the function of flight.

Behaviors can also be used to classify organisms, and, like other traits, can be the result of a synapomorphy or homoplasy. For example, the night-active primates, Lorises and Tarsiers, are not grouped together in Fig. 1.17. This is because their night-time behavior is not a synapomorphy (a shared derived character). In order for Lorises and Tarsiers to be included in the same monophyletic group, the group would need to be expanded to include lemurs with the tarsiers, monkeys, apes, and their last common ancestor (black dot).

As we learn more about genetics, and evolution, it is important to continue to explore and reassess relationships between organisms. Ideas about relationships need to be re-evaluated as discoveries are made and new information is found. Science isn't always about having the right answer, but rather about methodically searching for the best answer!

Molecular Phylogenies

Advances in biotechnology now allow scientists to use molecular characteristics to organize organisms. Just as scientists use DNA "fingerprints" to assess relatedness of humans in paternity tests, scientists can use genetic markers to assess relatedness of different species.

Molecular phylogenies are made by examining the differences in the DNA sequence of the organisms being compared. There are many genetic similarities between organisms. For example, human and mouse genes have a similarity of about 85 percent, and human and chimpanzee genes have about 96 percent similarity. For this reason, it is easier to study differences in genetics rather than similarities.

For scientists to gain information about relationships between widely diverse species (like those from different domains or kingdoms) they use genes that are similar. **Conserved genes** are genes that have not changed much over evolutionary time. These include the genes that make up ribosomal RNA (rRNA). Segments of rRNA genes, like the one identified as 16S from *E. coli* (a bacterium), corn (a plant), yeast (a fungus), and human (an animal), can be compared to see how well conserved the gene is.

Gene conservation usually occurs in functionally important genes because these types of genes are needed to assemble proteins essential to survival. **Coding regions** are segments of DNA that are translated to RNA and are important for the function of a gene or gene product. Note in Fig. 1.17 that regions of conservation are highlighted in yellow.

The conserved parts of the 16S rRNA gene are the places that provide information about the relationships between the organisms being compared (Fig. 1.18). In this case, *E. coli* has many different genetic bases compared to the other organisms, indicating that it is less closely related to them than they are to one another. This is not unexpected since *E. coli* is classified in a completely different domain than the other three groups in this example (animals, fungi, and plants).

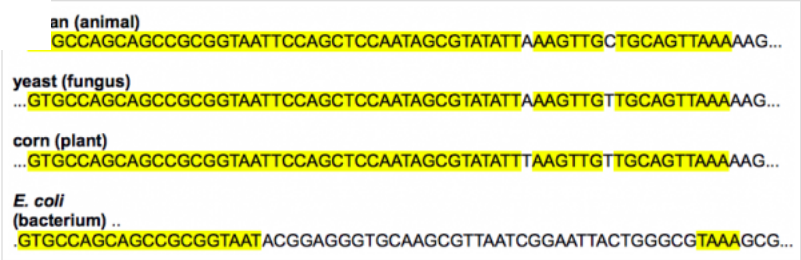

Fig. 1.18. Comparison of 16S ribosomsal RNA (rRNA) genes across four different types of organisms. Highlighted areas are regions of conservation. Note that this gene is conserved across multiple species, showing its importance in cellular function.

Non-coding regions are segments of DNA that are not translated to RNA. These non-coding regions are not considered functional parts of genes. However, non-coding regions do play a role within the cell. These non-coding regions of DNA are known as **introns**. They are areas where less conservation and more genetic mutation is expected. Scientists use introns to examine how organisms have changed over time. The rate of change over time can give clues as to how long ago organisms diverged from each other in a phylogenetic sense.

QUESTION SET

Classification of Life

FURTHER INVESTIGATIONS

Classification of Life

Useful Links

Alternate phylogenetic tree example image:

- Phylogenetic Groups

or more broadly:

- Partial Evolutionary Tree of the Vertebrates
- Whales

An activity on genetic variation:

- Genetic Variation by Nicholas J. Caruso

Many cool open-source videos of protozoan microbes:

- Wikipedia Euglena Video Gallery

Share and Connect

Share your activity modifications, ask for help, or read what other educators have to say

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